

SEQUENCE LISTING

<110> He, et al.

<120> Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 and 4

<130> PF140P1D2

<140> To Be Assigned

<141> 2004-03-17

<150> 09/613,508

<151> 2000-07-10

<150> 08/462,969

<151> 1995-06-05

<150> 08/334,251

<151> 1994-11-01

<160> 14

<170> PatentIn version 3.2

<210> 1

<211> 1369

<212> DNA

<213> Homo sapiens

<400> 1

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gcggggacac gggtcgcttt gggctcttcc acccctgcgg agcgactac cccgagccag	180
gggcggtgca agccccgccc ggccctaccc agggcggttc ctccctccgc agcgccgaga	240
cttttagttt cgcttttcgct aaaggggccc cagacccttg ctgcgagagc acggagagag	300
actgtgccag tcccagccgc cctaccgccg tgggaacgat ggcagatgat cagggctgta	360
ttgaagagca gggggttgag gattcagcaa atgaagattc agtggatgct aagccagacc	420
ggtcctcggt tgtaccgtcc ctcttcagta agaagaagaa aaatgtcacc atgcgatcca	480
tcaagaccac cggggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg	540
gcaaatgcat cataataaac aacaagaact ttgataaagt gacaggtatg ggcgttcgaa	600
acggaacaga caaagatgcc gaggcgtctt tcaagtgctt ccgaagcctg gggtttgacg	660
tgattgtcta taatgactgc tcttgtgcca agatgcaaga tctgcttaaa aaagcttctg	720
aagaggacca tacaatgcc gcctgcttcg cctgcctcct ctttaagccat ggagaagaaa	780
atgtaattta tgggaaagat ggtgtcacac caataaagga tttgacagcc cactttaggg	840
gggatagatg caaaaccctt ttagagaaac ccaaactctt cttcattcag gcttgccgag	900

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ggaccgagct tgatgatgcc atccaggccg actcggggcc catcaatgac acagatgcta      960
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gctattactc gtggaggagc ccaggaagag gctcctgggt tgtgcaagcc ctctgctcca    1080
tcctggagga gcacggaaaa gacctggaaa tcatgcagat cctcaccagg gtgaatgaca    1140
gagttgccag gcactttgag tctcagtctg atgaccaca cttccatgag aagaagcaga    1200
tcccctgtgt ggtctccatg ctcaccaagg aactctactt cagtcaatag ccatatcagg    1260
ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc    1320
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<210>  2
<211> 303
<212>  PRT
<213>  Homo sapiens

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<400>  2

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Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser
1              5              10              15

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Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val
              20              25              30

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Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile
              35              40              45

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Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
50              55              60

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Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
65              70              75              80

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Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
              85              90              95

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Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
              100              105              110

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Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
              115              120              125

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Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
130              135              140

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Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
145 150 155 160

Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
165 170 175

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
180 185 190

Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
195 200 205

Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser
210 215 220

Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp
225 230 235 240

Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu
245 250 255

Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His
260 265 270

Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile
275 280 285

Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
290 295 300

<210> 3
<211> 1159
<212> DNA
<213> Homo sapiens

<400> 3
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gccgtgagga gttagcgagc cctgctcaca ctggcgctc tggttttcgg tgggtgtgcc 180
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 cgttgtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720
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 ataccagtgg aggccgactt cttgtatgca tactccacag cacctgggta ttattcttgg 840
 cgaaattcaa aggatggctc ctggttcatc cagtcgcttt gtgccatgct gaaacagtat 900
 gccgacaagc ttgaatttat gcacattctt acccggggta accgaaagggt ggcaacagaa 960
 tttgagtcct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt 1020
 tccatgctca caaaagaact ctatttttat cactaaagaa atgggttggtt ggtggttttt 1080
 tttagtttgt atgccaagtg agaagatggt atatttgggt actgtatttc cctctcattg 1140
 gggacctact ctcatgctg 1159

<210> 4
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
 1 5 10 15

Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
 20 25 30

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
 35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
 50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
 65 70 75 80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
 85 90 95

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser

100					105					110					
Ser	Phe	Val	Cys	Val	Leu	Leu	Ser	His	Gly	Glu	Glu	Gly	Ile	Ile	Phe
		115					120					125			
Gly	Thr	Asn	Gly	Pro	Val	Asp	Leu	Lys	Lys	Ile	Thr	Asn	Phe	Phe	Arg
	130					135					140				
Gly	Asp	Arg	Cys	Arg	Ser	Leu	Thr	Gly	Lys	Pro	Lys	Leu	Phe	Ile	Ile
145					150					155					160
Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Cys	Gly	Ile	Glu	Thr	Asp	Ser
				165					170					175	
Gly	Val	Asp	Asp	Asp	Met	Ala	Cys	His	Lys	Ile	Pro	Val	Glu	Ala	Asp
			180					185					190		
Phe	Leu	Tyr	Ala	Tyr	Ser	Thr	Ala	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Asn
	195						200					205			
Ser	Lys	Asp	Gly	Ser	Trp	Phe	Ile	Gln	Ser	Leu	Cys	Ala	Met	Leu	Lys
	210					215					220				
Gln	Tyr	Ala	Asp	Lys	Leu	Glu	Phe	Met	His	Ile	Leu	Thr	Arg	Val	Asn
225					230					235					240
Arg	Lys	Val	Ala	Thr	Glu	Phe	Glu	Ser	Phe	Ser	Phe	Asp	Ala	Thr	Phe
				245					250					255	
His	Ala	Lys	Lys	Gln	Ile	Pro	Cys	Ile	Val	Ser	Met	Leu	Thr	Lys	Glu
			260					265					270		
Leu	Tyr	Phe	Tyr	His											
		275													

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a Bam HI restriction enzyme site (underlined) followed by 18 nucleotides of ICE-LAP-3 coding sequence starting from the presumed terminal amino acid of the processed protein codon

<400> 5
 gatcggatcc atgcgtgcgg ggacacgggt c

<210> 6
 <211> 31
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Contains complementary sequences to an Xba I site followed by 21
 nucleotides of ICE-LAP-3

 <400> 6
 gtactctaga tcattcaccc tggaggagga t 31

 <210> 7
 <211> 31
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Contains a Bam HI restriction enzyme site followed by 18
 nucleotides of ICE-LAP-4 coding sequence starting from the
 presumed terminal amino acid of the processed protein codon

 <400> 7
 gatcggtacc atggagaaca ctgaaaactc a 31

 <210> 8
 <211> 31
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Contains complementary sequences to an Xba I site followed by 21
 nucleotides of ICE-LAP-4

 <400> 8
 gtactctaga ttagtgataa aaatagagtt c 31

 <210> 9
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Contains the ICE-LAP-3 translational initiation site ATG followed
 by 5 nucleotides of ICE-LAP-3 coding sequence starting from the
 initiation codon

 <400> 9
 gactatgcgt gcggggacac gg 22

 <210> 10
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-3 coding sequence, not including the stop codon

<400> 10
 aatcaagcgt agtctgggac gtcgtatggg tattcacctt ggtggaggat ttg 53

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains the ICE-LAP-4 translational initiation site, ATG, followed by 15 nucleotides of ICE-LAP-4 coding sequence starting from the initiation codon

<400> 11
 accatggaga aactgaaaa c 21

<210> 12
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-4 coding sequence, not including the stop codon

<400> 12
 aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt 53

<210> 13
 <211> 503
 <212> PRT
 <213> Caenorhabditis elegans

<400> 13

Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
 1 5 10 15

Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala
 20 25 30

Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
 35 40 45

Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
 50 55 60

Gly Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly
 65 70 75 80

His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp
 85 90 95

Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg
 100 105 110

Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val
 115 120 125

His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp
 130 135 140

Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser
 145 150 155 160

Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser
 165 170 175

Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly
 180 185 190

Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr
 195 200 205

Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr
 210 215 220

Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser
 225 230 235 240

Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met
 245 250 255

Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu
 260 265 270

Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly
 275 280 285

Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His
 290 295 300

Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val
 305 310 315 320

Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp
 325 330 335

Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile
 340 345 350

Val Phe Val Gln Ala Cys Arg Gly Glu Arg Arg Asp Asn Gly Phe Pro
 355 360 365

Val Leu Asp Ser Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp
 370 375 380

Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro
 385 390 395 400

Gln Val Gln Gln Val Trp Arg Lys Lys Pro Ser Gln Ala Asp Ile Leu
 405 410 415

Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val Ser Trp Arg Asn Ser Ala
 420 425 430

Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His
 435 440 445

Ala Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys
 450 455 460

Val Ala Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln
 465 470 475 480

Met Pro Glu Met Thr Ser Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro
 485 490 495

Glu Ala Arg Asn Ser Ala Val
 500

<210> 14
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 14

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			20					25						30			
Arg	Val	Leu	Asn	Lys	Glu	Glu	Met	Glu	Lys	Val	Lys	Arg	Glu	Asn	Ala		
		35					40					45					
Thr	Val	Met	Asp	Lys	Thr	Arg	Ala	Leu	Ile	Asp	Ser	Val	Ile	Pro	Lys		
	50					55					60						
Gly	Ala	Gln	Ala	Cys	Gln	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp		
65					70					75					80		
Ser	Tyr	Leu	Ala	Gly	Thr	Leu	Gly	Leu	Ser	Ala	Asp	Gln	Thr	Ser	Gly		
				85					90					95			
Asn	Tyr	Leu	Asn	Met	Gln	Asp	Ser	Gln	Gly	Val	Leu	Ser	Ser	Phe	Pro		
			100					105						110			
Ala	Pro	Gln	Ala	Val	Gln	Asp	Asn	Pro	Ala	Met	Pro	Thr	Ser	Ser	Gly		
		115					120							125			
Ser	Glu	Gly	Asn	Val	Lys	Leu	Cys	Ser	Leu	Glu	Glu	Ala	Gln	Arg	Ile		
	130					135						140					
Trp	Lys	Gln	Lys	Ser	Ala	Glu	Ile	Tyr	Pro	Ile	Met	Asp	Lys	Ser	Ser		
145					150					155					160		
Arg	Thr	Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Glu	Glu	Phe	Asp	Ser	Ile		
			165						170					175			
Pro	Arg	Arg	Thr	Gly	Ala	Glu	Val	Asp	Ile	Thr	Gly	Met	Thr	Met	Leu		
			180					185					190				
Leu	Gln	Asn	Leu	Gly	Tyr	Ser	Val	Asp	Val	Lys	Lys	Asn	Leu	Thr	Ala		
		195					200					205					
Ser	Asp	Met	Thr	Thr	Glu	Leu	Glu	Ala	Phe	Ala	His	Arg	Pro	Glu	His		
	210					215					220						
Lys	Thr	Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Arg		
225					230					235					240		
Glu	Gly	Ile	Cys	Gly	Lys	Lys	His	Ser	Glu	Gln	Val	Pro	Asp	Ile	Leu		

				245						250					255
Gln	Leu	Asn	Ala	Ile	Phe	Asn	Met	Leu	Asn	Thr	Lys	Asn	Cys	Pro	Ser
			260					265					270		
Leu	Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Ile	Gln	Ala	Cys	Arg	Gly	Asp
		275					280					285			
Ser	Pro	Gly	Val	Val	Trp	Phe	Lys	Asp	Ser	Val	Gly	Val	Ser	Gly	Asn
	290					295					300				
Leu	Ser	Leu	Pro	Thr	Thr	Glu	Glu	Phe	Glu	Asp	Asp	Ala	Ile	Lys	Lys
305					310					315					320
Ala	His	Ile	Glu	Lys	Asp	Phe	Ile	Ala	Phe	Cys	Ser	Ser	Thr	Pro	Asp
				325					330					335	
Asn	Val	Ser	Trp	Arg	His	Pro	Thr	Met	Gly	Ser	Val	Phe	Ile	Gly	Arg
			340					345					350		
Leu	Ile	Glu	His	Met	Gln	Glu	Tyr	Ala	Cys	Ser	Cys	Asp	Val	Glu	Glu
		355					360					365			
Ile	Phe	Arg	Lys	Val	Arg	Phe	Ser	Phe	Glu	Gln	Pro	Asp	Gly	Arg	Ala
	370					375					380				
Gln	Met	Pro	Thr	Thr	Glu	Arg	Val	Thr	Leu	Thr	Arg	Cys	Phe	Tyr	Leu
385					390					395					400
Phe	Pro	Gly	His												